

SEQUENCE LISTING

<110> Zhang, Lian Hui

Lin, Yi Han

Xu, Jin Ling

<120> RALSTONIA AHL-ACYLASE GENE

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<170> PatentIn version 3.0

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			500					505					510			
Pro	Arg	Ile	Leu	Gly	Asn	Glu	Arg	Thr	Pro	Arg	Ser	Leu	Arg	Thr	Arg	
		515					520					525				
Leu	Gly	Leu	Asp	Gln	Ile	Gln	Gln	Arg	Leu	Ala	Gly	Thr	Asp	Gly	Leu	
	530					535					540					

Pro	Gly	Lys	Gly	Phe	Thr	Thr	Ala	Arg	Leu	Trp	Gln	Val	Met	Phe	Gly	545	550	555	560
Asn	Arg	Met	His	Gly	Ala	Glu	Leu	Val	Arg	Asp	Asp	Leu	Val	Ala	Leu	565	570	575	
Cys	Arg	Arg	Gln	Pro	Thr	Ala	Thr	Ala	Ser	Asn	Gly	Ala	Ile	Val	Asp	580	585	590	
Leu	Thr	Ala	Ala	Cys	Thr	Ala	Leu	Ser	Arg	Phe	Asp	Glu	Arg	Ala	Asp	595	600	605	
Leu	Asp	Ser	Arg	Gly	Ala	His	Leu	Phe	Thr	Glu	Phe	Leu	Ala	Gly	Gly	610	615	620	
Ile	Arg	Phe	Ala	Asp	Thr	Phe	Glu	Val	Thr	Asp	Pro	Val	Arg	Thr	Pro	625	630	635	640
Ala	Pro	Phe	Trp	Asn	Thr	Thr	Asp	Pro	Arg	Val	Arg	Thr	Ala	Leu	Ala	645	650	655	
Asp	Ala	Cys	Asn	Gly	Ser	Pro	Ala	Ser	Pro	Ser	Thr	Arg	Ser	Val	Gly	660	665	670	
Asp	Ile	His	Thr	Asp	Ser	Arg	Gly	Glu	Arg	Arg	Ile	Pro	Ile	His	Gly	675	680	685	
Gly	Arg	Gly	Glu	Ala	Gly	Thr	Phe	Asn	Val	Ile	Thr	Asn	Pro	Leu	Val	690	695	700	
Pro	Gly	Val	Gly	Tyr	Pro	Gln	Val	Val	His	Gly	Thr	Ser	Phe	Val	Met	705	710	715	720
Ala	Val	Glu	Leu	Gly	Pro	His	Gly	Pro	Ser	Gly	Arg	Gln	Ile	Leu	Thr	725	730	735	
Tyr	Ala	Gln	Ser	Thr	Asn	Pro	Asn	Ser	Pro	Trp	Tyr	Ala	Asp	Gln	Thr	740	745	750	
Val	Leu	Tyr	Ser	Arg	Lys	Gly	Trp	Asp	Thr	Ile	Lys	Tyr	Thr	Glu	Ala	755	760	765	
Gln	Ile	Ala	Ala	Asp	Pro	Asn	Leu	Arg	Val	Tyr	Arg	Val	Ala	Gln	Arg	770	775	780	
Gly	Arg															785			

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<211> 777

<212> PRT

<213> P. aeruginosa

<400> 5

Met	Ser	Arg	Pro	Phe	Arg	Pro	Pro	Leu	Cys	Arg	Glu	Thr	Thr	Ser	Met	1	5	10	15
Gly	Met	Arg	Thr	Val	Leu	Thr	Gly	Leu	Ala	Gly	Met	Leu	Leu	Gly	Ser	20	25	30	
Met	Met	Pro	Val	Gln	Ala	Asp	Met	Pro	Arg	Pro	Thr	Gly	Leu	Ala	Ala	35	40	45	
Asp	Ile	Arg	Trp	Thr	Ala	Tyr	Gly	Val	Pro	His	Ile	Arg	Ala	Lys	Asp	50	55	60	
Glu	Arg	Gly	Leu	Gly	Tyr	Gly	Ile	Gly	Tyr	Ala	Tyr	Ala	Arg	Asp	Asn	65	70	75	
Ala	Cys	Leu	Leu	Ala	Glu	Glu	Ile	Val	Thr	Ala	Arg	Gly	Glu	Arg	Ala	85	90	95	
Arg	Tyr	Phe	Gly	Ser	Glu	Gly	Lys	Ser	Ser	Ala	Glu	Leu	Asp	Asn	Leu	100	105	110	
Pro	Ser	Asp	Ile	Phe	Tyr	Ala	Trp	Leu	Asn	Gln	Pro	Glu	Ala	Leu	Gln	115	120	125	
Ala	Phe	Trp	Gln	Ala	Gln	Thr	Pro	Ala	Val	Arg	Gln	Leu	Leu	Glu	Gly	130	135	140	
Tyr	Ala	Ala	Gly	Phe	Asn	Arg	Phe	Leu	Arg	Glu	Ala	Asp	Gly	Lys	Thr	145	150	155	
Thr	Ser	Cys	Leu	Gly	Gln	Pro	Trp	Leu	Arg	Ala	Ile	Ala	Thr	Asp	Asp	165	170	175	
Leu	Leu	Arg	Leu	Thr	Arg	Arg	Leu	Leu	Val	Glu	Gly	Gly	Val	Gly	Gln	180	185	190	
Phe	Ala	Asp	Ala	Leu	Val	Ala	Ala	Ala	Pro	Pro	Gly	Ala	Glu	Lys	Val	195	200	205	
Ala	Leu	Ser	Gly	Glu	Gln	Ala	Phe	Gln	Val	Ala	Glu	Gln	Arg	Arg	Gln	210	215	220	
Arg	Phe	Arg	Leu	Glu	Arg	Gly	Ser	Asn	Ala	Ile	Ala	Val	Gly	Ser	Glu	225	230	235	
																240			

Arg Ser Ala Asp Gly Lys Gly Met Leu Leu Ala Asn Pro His Phe Pro
 245 250 255
 Trp Asn Gly Ala Met Arg Phe Tyr Gln Met His Leu Thr Ile Pro Gly
 260 265 270
 Arg Leu Asp Val Met Gly Ala Ser Leu Pro Gly Leu Pro Val Val Asn
 275 280 285
 Ile Gly Phe Ser Arg His Leu Ala Trp Thr His Thr Val Asp Thr Ser
 290 295 300
 Ser His Phe Thr Leu Tyr Arg Leu Ala Leu Asp Pro Lys Asp Pro Arg
 305 310 315 320
 Arg Tyr Leu Val Asp Gly Arg Ser Leu Pro Leu Glu Glu Lys Ser Val
 325 330 335
 Ala Ile Glu Val Arg Gly Ala Asp Gly Lys Leu Ser Arg Val Glu His
 340 345 350
 Lys Val Tyr Gln Ser Ile Tyr Gly Pro Leu Val Val Trp Pro Gly Lys
 355 360 365
 Leu Asp Trp Asn Arg Ser Glu Ala Tyr Ala Leu Arg Asp Ala Asn Leu
 370 375 380
 Glu Asn Thr Arg Val Leu Gln Gln Trp Tyr Ser Ile Asn Gln Ala Ser
 385 390 395 400
 Asp Val Ala Asp Leu Arg Arg Arg Val Glu Ala Leu Gln Gly Ile Pro
 405 410 415
 Trp Val Asn Thr Leu Ala Ala Asp Glu Gln Gly Asn Ala Leu Tyr Met
 420 425 430
 Asn Gln Ser Val Val Pro Tyr Leu Lys Pro Glu Leu Ile Pro Ala Cys
 435 440 445
 Ala Ile Pro Gln Leu Val Ala Glu Gly Leu Pro Ala Leu Gln Gly Gln
 450 455 460
 Asp Ser Arg Cys Ala Trp Ser Arg Asp Pro Ala Ala Ala Gln Ala Gly
 465 470 475 480
 Ile Thr Pro Ala Ala Gln Leu Pro Val Leu Leu Arg Arg Asp Phe Val
 485 490 495
 Gln Asn Ser Asn Asp Ser Ala Trp Leu Thr Asn Pro Ala Ser Pro Leu
 500 505 510
 Gln Gly Phe Ser Pro Leu Val Ser Gln Glu Lys Pro Ile Gly Pro Arg
 515 520 525
 Ala Arg Tyr Ala Leu Ser Arg Leu Gln Gly Lys Gln Pro Leu Glu Ala
 530 535 540

Lys Thr Leu Glu Glu Met Val Thr Ala Asn His Val Phe Ser Ala Asp
 545 550 555 560
 Gln Val Leu Pro Asp Leu Leu Arg Leu Cys Arg Asp Asn Gln Gly Glu
 565 570 575
 Lys Ser Leu Ala Arg Ala Cys Ala Ala Leu Ala Gln Trp Asp Arg Gly
 580 585 590
 Ala Asn Leu Asp Ser Gly Ser Gly Phe Val Tyr Phe Gln Arg Phe Met
 595 600 605
 Gln Arg Phe Ala Glu Leu Asp Gly Ala Trp Lys Glu Pro Phe Asp Ala
 610 615 620
 Gln Arg Pro Leu Asp Thr Pro Gln Gly Ile Ala Leu Asp Arg Pro Gln
 625 630 635 640
 Val Ala Thr Gln Val Arg Gln Ala Leu Ala Asp Ala Ala Ala Glu Val
 645 650 655
 Glu Lys Ser Gly Ile Pro Asp Gly Ala Arg Trp Gly Asp Leu Gln Val
 660 665 670
 Ser Thr Arg Gly Gln Glu Arg Ile Ala Ile Pro Gly Gly Asp Gly His
 675 680 685
 Phe Gly Val Tyr Asn Ala Ile Gln Ser Val Arg Lys Gly Asp His Leu
 690 695 700
 Glu Val Val Gly Gly Thr Ser Tyr Ile Gln Leu Val Thr Phe Pro Glu
 705 710 715 720
 Glu Gly Pro Lys Ala Arg Gly Leu Leu Ala Phe Ser Gln Ser Ser Asp
 725 730 735
 Pro Arg Ser Pro His Tyr Arg Asp Gln Thr Glu Leu Phe Ser Arg Gln
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 Gln Leu Gln Arg Leu Ser Ile Arg Glu
 770 775

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<220>

<223> Forward Primer for the QsbA gene

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cgtggatcca tgatgcagga ttgccgctg cgc

33

<210> 7

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Reverse Primer for the QsbA gene

<400> 7

cgcgattca ccggcagccc tcatgcgaca ac

32